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<120> Fusion protein composition

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<150> P2003-350158
<151> 2003-10-08

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<170> PatentIn Ver. 2.1

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Gly Asp Lys Gly Lys Pro Arg Lys Val Ala Leu Ile Thr Gly Ile Thr
             20                  25                  30

ggc cag gat ggc tca tac ttg gca gaa ttc ctg ctg gag aaa gga tac   144
Gly Gln Asp Gly Ser Tyr Leu Ala Glu Phe Leu Leu Glu Lys Gly Tyr
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gag gtt cat gga att gta cgg cga tcc agt tca ttt aat aca ggt cga   192
Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg
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att gaa cat tta tat aag aat cca cag gct cat att gaa gga aac atg   240
Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu Gly Asn Met
 65                  70                  75                  80

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Lys Leu His Tyr Gly Asp Leu Thr Asp Ser Thr Cys Leu Val Lys Ile
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atc aat gaa gtc aaa cct aca gag atc tac aat ctt ggt gcc cag agc   336
Ile Asn Glu Val Lys Pro Thr Glu Ile Tyr Asn Leu Gly Ala Gln Ser
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cat gtc aag att tcc ttt gac tta gca gag tac act gca gat gtt gat   384
His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp
            120                 125                 130

gga gtt ggc acc ttg cgg ctt ctg gat gca att aag act tgt ggc ctt   432
Gly Val Gly Thr Leu Arg Leu Leu Asp Ala Ile Lys Thr Cys Gly Leu
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Lys Val Gln Glu Ile Pro Gln Lys Glu Thr Thr Pro Phe Tyr Pro Arg
165                 170                 175                 180

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Ser Pro Tyr Gly Ala Ala Lys Leu Tyr Ala Tyr Trp Ile Val Val Asn
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cat gag agt cct aga aga gga gct aat ttt gtt act cga aaa att agc   672
His Glu Ser Pro Arg Arg Gly Ala Asn Phe Val Thr Arg Lys Ile Ser
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cgg tca gta gct aag att tac ctt gga caa ctg gaa tgt ttc agt ttg   720
Arg Ser Val Ala Lys Ile Tyr Leu Gly Gln Leu Glu Cys Phe Ser Leu
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gga aat ctg gac gcc aaa cga gac tgg ggc cat gcc aag gac tat gtc   768
Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val
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gag gct atg tgg ctg atg tta caa aat gat gaa cca gag gac ttt gtc   816
Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
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Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
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ttc atg cac att gga aag acc att gtg tgg gaa gga aag aat gaa aat   912
Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
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gaa gtg ggc aga tgt aaa gag acc ggc aaa att cat gtg act gtg gat   960
Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
    310                 315                 320

ctg aaa tac tac cga cca act gaa gtg gac ttc ctg cag gga gac tgc   1008
Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
325                 330                 335                 340

tcc aag gcg cag cag aaa ctg aac tgg aag ccc cgc gtt gcc ttt gac   1056
Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
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gag ctg gtg agg gag atg gtg caa gcc gat gtg gag ctc atg aga acc   1104
Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr
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Asn Pro Asn Ala
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Lys	Leu	His	Tyr	Gly	Asp	Leu	Thr	Asp	Ser	Thr	Cys	Leu	Val	Lys	Ile
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Ile	Asn	Glu	Val	Lys	Pro	Thr	Glu	Ile	Tyr	Asn	Leu	Gly	Ala	Gln	Ser
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His	Val	Lys	Ile	Ser	Phe	Asp	Leu	Ala	Glu	Tyr	Thr	Ala	Asp	Val	Asp
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Gly	Val	Gly	Thr	Leu	Arg	Leu	Leu	Asp	Ala	Ile	Lys	Thr	Cys	Gly	Leu
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Lys	Val	Gln	Glu	Ile	Pro	Gln	Lys	Glu	Thr	Thr	Pro	Phe	Tyr	Pro	Arg
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Ser	Pro	Tyr	Gly	Ala	Ala	Lys	Leu	Tyr	Ala	Tyr	Trp	Ile	Val	Val	Asn
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Phe	Arg	Glu	Ala	Tyr	Asn	Leu	Phe	Ala	Val	Asn	Gly	Ile	Leu	Phe	Asn
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Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val
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Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
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Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
            280                 285                 290

Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
        295                 300                 305

Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
    310                 315                 320

Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
325                 330                 335                 340

Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
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tgctgcaatg gtaggaggcc ttttccggaa tatcaaatac aacttggatt tctggaggaa 360

gaatgtgcac atcaatgaca acgtcctgca ctcagctttc gaggtgggca ctcgcaaggt 420

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aatgatccac aatggtccac cccacagcag caattttggg tactcgtatg ccaagaggat 540

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ccctaccaat gtctttggac ctcatgacaa cttcaacatt gaagatggcc atgtgctgcc 660

tggcctcatc cataaggtgc atctggccaa gagtaatggt tcagccttga ctgtttgggg 720

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cacttttgat tcaacaaagt cagatgggca gtataagaag acagccagca atggcaagct 960

tcgggcctac ttgcctgatt tccgtttcac acccttcaag caggctgtga aggagacctg 1020

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Leu Pro Gly Glu Glu Trp Val Phe Val Ser Ser Lys Asp Ala Asp Leu
        35                  40                  45

Thr Asp Ala Ala Gln Thr Gln Ala Leu Phe Gln Lys Val Gln Pro Thr
    50                  55                  60

His Val Ile His Leu Ala Ala Met Val Gly Gly Leu Phe Arg Asn Ile
65                  70                  75                  80

Lys Tyr Asn Leu Asp Phe Trp Arg Lys Asn Val His Ile Asn Asp Asn
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Val Leu His Ser Ala Phe Glu Val Gly Thr Arg Lys Val Val Ser Cys
            100                 105                 110

Leu Ser Thr Cys Ile Phe Pro Asp Lys Thr Thr Tyr Pro Ile Asp Glu
        115                 120                 125

Thr Met Ile His Asn Gly Pro Pro His Ser Ser Asn Phe Gly Tyr Ser
    130                 135                 140

Tyr Ala Lys Arg Met Ile Asp Val Gln Asn Arg Ala Tyr Phe Gln Gln
145                 150                 155                 160

His Gly Cys Thr Phe Thr Ala Val Ile Pro Thr Asn Val Phe Gly Pro
                165                 170                 175

His Asp Asn Phe Asn Ile Glu Asp Gly His Val Leu Pro Gly Leu Ile
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180 185 190

His Lys Val His Leu Ala Lys Ser Asn Gly Ser Ala Leu Thr Val Trp
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210 215 220

Arg Leu Phe Ile Trp Val Leu Arg Glu Tyr Asn Glu Val Glu Pro Ile
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Ile Leu Ser Val Gly Glu Glu Asp Glu Val Ser Ile Lys Glu Ala Ala
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Glu Ala Val Val Glu Ala Met Asp Phe Cys Gly Glu Val Thr Phe Asp
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Ser Thr Lys Ser Asp Gly Gln Tyr Lys Lys Thr Ala Ser Asn Gly Lys
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Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
 65                  70                  75                  80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
                 85                  90                  95

Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Asp Leu Gly Lys Asp His
            100                 105                 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
        115                 120                 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Lys Leu Glu Gly Asn Glu
    130                 135                 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
145                 150                 155                 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
                165                 170                 175

Gly Glu Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
            180                 185                 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
        195                 200                 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
    210                 215                 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225                 230                 235                 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
                245                 250                 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
            260                 265                 270

Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
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Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
    290                 295                 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
305                 310                 315                 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
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Arg Pro Gln Pro Trp Leu Glu Arg Glu Ile Glu Glu Thr Thr Lys Lys
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    370                 375                 380

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385                 390                 395                 400

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
                405                 410                 415

Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
            420                 425                 430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
        435                 440                 445

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
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Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465                 470                 475                 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
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Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
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His Gln Pro Arg Thr Lys Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
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Ile Gly Val Ala Gly Asn His Trp Asn Gly Tyr Ser Lys Gly Val Asn
    530                 535                 540

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Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
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Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
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Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
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Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
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Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
        115                 120                 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
    130                 135                 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
145                 150                 155                 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
                165                 170                 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
            180                 185                 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
        195                 200                 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
    210                 215                 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225                 230                 235                 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
                245                 250                 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
            260                 265                 270

Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
        275                 280                 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
    290                 295                 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
305                 310                 315                 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
                325                 330                 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
            340                 345                 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
        355                 360                 365

Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
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    370                 375                 380

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385                 390                 395                 400

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Thr Leu Leu Lys Glu
                405                 410                 415

Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
            420                 425                 430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
        435                 440                 445

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
    450                 455                 460

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465                 470                 475                 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
                485                 490                 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
            500                 505                 510

His Lys Pro Arg Thr Glu Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
        515                 520                 525

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
    530                 535                 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545                 550                 555                 560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
                565                 570


<210> 9
<211> 5
<212> PRT
<213> Mus musculus

<400> 9□@
Asp His Ala Ile His
  1               5


<210> 10
<211> 17
<212> PRT
<213> Mus musculus

<400> 10□@
Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe Lys
  1               5                  10                  15

Gly
<210> 11
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<211> 6
<212> PRT
<213> Mus musculus

<400> 11□@
Ser Leu Asn Met Ala Tyr
1 5

<210> 12
<211> 17
<212> PRT
<213> Mus musculus

<400> 12□@
Lys Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 13
<211> 7
<212> PRT
<213> Mus musculus

<400> 13□@
Trp Ala Ser Ala Arg Glu Ser
1 5

<210> 14
<211> 9
<212> PRT
<213> Mus musculus

<400> 14□@
Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr
1 5

<210> 15
<211> 115
<212> PRT
<213> Mus musculus□@

<400> 15
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

```
 65                  70                  75                  80

Val Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                 85                  90                  95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
            100                 105                 110

Val Ser Ser
        115


<210> 16
<211> 113
<212> PRT
<213> Mus musculus□@

<400> 16
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Pro Val Ser Val Gly
  1               5                  10                  15

Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
             20                  25                  30

Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
         35                  40                  45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val
     50                  55                  60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser
 65                  70                  75                  80

Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                 85                  90                  95

Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Val Leu
            100                 105                 110

Lys


<210> 17
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Amino Acid Sequence of Single Chain
Antibody

<400> 17
Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
  1               5                  10                  15

Val His Ser Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys
             20                  25                  30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
         35                  40                  45
```

```
Thr Asp His Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu
     50                  55                  60

Glu Trp Ile Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn
 65                  70                  75                  80

Glu Arg Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                 85                  90                  95

Thr Ala Tyr Val Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

Tyr Phe Cys Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr
        115                 120                 125

Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gly Gly Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu
145                 150                 155                 160

Pro Val Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln
                165                 170                 175

Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln
            180                 185                 190

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala
        195                 200                 205

Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
    210                 215                 220

Asp Phe Thr Leu Ser Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val
225                 230                 235                 240

Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly
                245                 250                 255

Thr Lys Leu Val Leu Lys Arg Ala Ala
            260                 265
```

<210> 18
<211> 463
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 18
ccggaattcg acccctcacc atggaatgga gctgggtctt tctcttcttc ctgtcagtaa 60

ctacaggtgt ccactcccag gttcagttgc agcagtctga cgctgagttg gtgaaacctg 120

gggcttcagt gaagatttcc tgcaaggctt ctggctacac cttcactgac catgcaattc 180

actgggtgaa acagaaccct gaacagggcc tggaatggat tggatatttt tctcccggaa 240

atgatgattt taaatacaat gagaggttca agggcaaggc cacactgact gcagacaaat 300

cctccagcac tgcctacgtg cagctcaaca gcctgacatc tgaggattct gcagtgtatt 360

tctgtaccag atccctgaat atggcctact ggggtcaagg aacctcagtc accgtctcct 420

caggtggcgg aggcagcgga ggcggtggct ccggaactag tcc 463

<210> 19
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 19
ccggaattcg acccctcacc atggaatgga gctgggtctt tctcttcttc ctgtcagtaa 60

ctacaggtgt ccactcccag gttcagttgc agcagtctga cgctgagttg gtgaaacctg 120

gggcttcag 129

<210> 20
<211> 134
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 20
catttccggg agaaaaatat ccaatccatt ccaggccctg ttcagggttc tgtttcaccc 60

agtgaattgc atggtcagtg aaggtgtagc cagaagcctt gcaggaaatc ttcactgaag 120

ccccaggttt cacc 134

<210> 21
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 21
ggatattttt ctcccggaaa tgatgatttt aaatacaatg agaggttcaa gggcaaggcc 60

acactgactg cagacaaatc ctccagcact gcctacgtgc agctcaacag cctgacatct 120

gaggattctg c 131

<210> 22
<211> 132

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 22
ggactagttc cggagccacc gcctccgctg cctccgccac ctgaggagac ggtgactgag 60

gttccttgac cccagtaggc catattcagg gatctggtac agaaatacac tgcagaatcc 120

tcagatgtca gg 132

<210> 23
<211> 536
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 23□@□@
ccggaattct ccggaggcgg aggctcggac attgtgatgt cacagtctcc atcctcccta 60

cctgtgtcag ttggcgagaa ggttactttg agctgcaagt ccagtcagag ccttttatat 120

agtggtaatc aaaagaacta cttggcctgg taccagcaga aaccagggca gtctcctaaa 180

ctgctgattt actgggcatc cgctagggaa tctggggtcc ctgatcgctt cacaggcagt 240

ggatctggga cagatttcac tctctccatc agcagtgtga agactgaaga cctggcagtt 300

tattactgtc agcagtatta tagctatccc ctcacgttcg gtgctgggac caagctggtg 360

ctgaaacggg ccgccgagcc caaatctcct gacaaaactc acacgtgccc accgtgccca 420

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgac tagtcc 536

<210> 24
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 24
tctgaattct ccggaggcgg aggctcggac attgtgatgt cacagtctcc atcctcccta 60

cctgtgtcag ttggcgagaa ggttactttg agctgcaagt ccagtcagag ccttttatat 120

agtggtaatc aaaagaacta cttggcctgg 150

<210> 25

<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 25
cacactgctg atggagagag tgaaatctgt cccagatcca ctgcctgtga agcgatcagg 60

gaccccagat tccctagcgg atgcccagta aatcagcagt ttaggagact gccctggttt 120

ctgctggtac caggccaagt agttcttttg 150

<210> 26
<211> 149
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 26
ctctctccat cagcagtgtg aagactgaag acctggcagt ttattactgt cagcagtatt 60

atagctatcc cctcacgttc ggtgctggga ccaagctggt gctgaaacgg gccgccgagc 120

ccaaatctcc tgacaaaact cacacgtgc 149

<210> 27
<211> 149
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 27
ggactagtca cgtccaccac cacgcatgtg acctcagggg tccgggagat catgagggtg 60

tccttgggtt ttgggggggaa gaggaagact gacggtcccc ccaggagttc aggtgctggg 120

cacggtgggc acgtgtgagt tttgtcagg 149

<210> 28
<211> 526
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 28
caggaaacag ctatgacggt accgaattcg cgaggcaggc agcctggaga gaaggcgctg 60

ggctgcgagg gcgcgagggc gcgagggcag ggggcaaccg gaccccgccc gcatccatgg 120

cgcccgtcgc cgtctgggcc gcgctggccg tcggactgga gctctgggct gcggcgcacg 180

ccttgcccgc ccaggtggca tttacaccct acgccccgga gcccgggagc acatgccggc 240

tcagagaata ctatgaccag acagctcaga tgtgctgcag caaatgctcg ccgggccaac 300

atgcaaaagt cttctgtacc aagacctcgg acaccgtgtg tgactcctgt gaggacagca 360

catacaccca gctctggaac tgggttcccg agtgcttgag ctgtggctcc cgctgtagct 420

ctgaccaggt ggaaactcaa gcctgcactc gggaacagaa ccgcatctgc acctgcaggc 480

ccggctggta ctgcgcgctg agcaagctta ctggccgtcg ttttac 526

<210> 29
<211> 537
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 29
caggaaacag ctatgacggt accgctgagc aagcaggagg ggtgccggct gtgcgcgccg 60

ctgcgcaagt gccgcccggg cttcggcgtg gccagaccag gaactgaaac atcagacgtg 120

gtgtgcaagc cctgtgcccc ggggacgttc tccaacacga cttcatccac ggatatttgc 180

aggccccacc agatctgtaa cgtggtggcc atccctggga atgcaagcat ggatgcagtc 240

tgcacgtcca cgtcccccac ccggagtatg gccccagggg cagtacactt accccagcca 300

gtgtccacac gatcccaaca cacgcagcca actccagaac ccagcactgc tccaagcacc 360

tccttcctgc tcccaatggg ccccagcccc ccagctgaag ggagcactgg cgacgagccc 420

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 480

ccgtcagtct tcctcttccc cccaaaaccc aaggaagctt actggccgtc gttttac 537

<210> 30
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 30
atggcgcccg tcgccgtctg ggccgcgctg gccgtcggac tggagctctg ggctgcggcg 60

cacgccttgc ccgcccaggt ggcatttaca ccctacgccc cggagcccgg gagcacatgc 120

cggctcagag aatactatga ccagacagct 150

<210> 31
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 31
agacggcgac gggcgccatg gatgcgggcg gggtccggtt gccccctgcc ctcgcgccct 60

cgcgccctcg cagcccagcg ccttctctcc aggctgcctg cctcgcgaat tcggtaccgt 120

catagctgtt tcctg 135

<210> 32
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 32
gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt agctctgacc aggtggaaac 60

tcaagcctgc actcgggaac agaaccgcat ctgcacctgc aggcccggct ggtactgcgc 120

gctgagcaag cttactggcc gtcgttttac 150

<210> 33
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 33
gcactcggga acccagttcc agagctgggt gtatgtgctg tcctcacagg agtcacacac 60

ggtgtccgag gtcttggtac agaagacttt tgcatgttgg cccggcgagc atttgctgca 120

gcacatctga gctgtctggt catagtattc 150

<210> 34
<211> 149
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 34

ctgtgccccg gggacgttct ccaacacgac ttcatccacg gatatttgca ggccccacca 60

gatctgtaac gtggtggcca tccctgggaa tgcaagcatg gatgcagtct gcacgtccac 120

gtcccccacc cggagtatgg ccccagggg 149

<210> 35
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 35
gaacgtcccc ggggcacagg gcttgcacac cacgtctgat gtttcagttc ctggtctggc 60

cacgccgaag cccgggcggc acttgcgcag cggcgcgcac agccggcacc cctcctgctt 120

gctcagcggt accgtcatag ctgtttcctg 150

<210> 36
<211> 145
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 36
agctgaaggg agcactggcg acgagcccaa atcttgtgac aaaactcaca catgcccacc 60

gtgcccagca cctgaactcc tgggggggacc gtcagtcttc ctcttccccc caaaacccaa 120

ggaagcttac tggccgtcgt tttac 145

<210> 37
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 37
gccagtgctc ccttcagctg gggggctggg gcccattggg agcaggaagg aggtgcttgg 60

agcagtgctg ggttctggag ttggctgcgt gtgttgggat cgtgtggaca ctggctgggg 120

taagtgtact gcccctgggg ccatactccg 150

<210> 38
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 38
caggaaacag ctatgacggt accgaattcc gacgagccat ggttgctggg agcgacgcgg 60

ggcgggccct gggggtcctc agcgtggtct gcctgctgca ctgctttggt ttcatcagct 120

gtttttccca acaaatatat ggtgttgtgt atgggaatgt aactttccat gtaccaagca 180

atgtgccttt aaaagaggtc ctatggaaaa aacaaaagga taaagttgca gaactggaaa 240

attctgaatt cagagctttc tcatctttta aaaatagggt ttatttagac actgtgtcag 300

gtagcctcac tatctacaac ttaacatcat cagatgaaga tgagtatgaa atggaatcgc 360

caaatattac tgataccatg aagttctttc tttatgtcga caaaactcac acatgcccac 420

cgtgcccagc acctgactgg ccgtcgtttt ac 452

<210> 39
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 39
gtttcatcag ctgtttttcc caacaaatat atggtgttgt gtatgggaat gtaactttcc 60

atgtaccaag caatgtgcct ttaaaagagg tcctatggaa aaaacaaaag gataaagttg 120

cagaactgga aaattctg 138

<210> 40
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 40
gggaaaaaca gctgatgaaa ccaaagcagt gcagcaggca gaccacgctg aggaccccca 60

gggcccgccc cgcgtcgctc ccagcaacca tggctcgtcg gaattcggta ccgtcatagc 120

tgtttcctg 129

<210> 41
<211> 133
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 41
cttaacatca tcagatgaag atgagtatga aatggaatcg ccaaatatta ctgataccat 60

gaagttcttt ctttatgtcg acaaaactca cacatgccca ccgtgcccag cacctgactg 120

gccgtcgttt tac 133

<210> 42
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 42
catcttcatc tgatgatgtt aagttgtaga tagtgaggct acctgacaca gtgtctaaat 60

aaaccctatt tttaaaagat gagaaagctc tgaattcaga attttccagt tctgcaac 118

<210> 43
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 43
gtaaaacgac ggccagt 17

<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 44
taaatagaat tcggcatcat gtggcagctg ct 32

<210> 45
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 45
aataaaggat cctggggtca tttgtcttga gggt 34

<210> 46

<211> 788
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (13)..(774)

<400> 46
gaattcggca tc atg tgg cag ctg ctc ctc cca act gct ctg cta ctt cta 51
Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu
1 5 10

gtt tca gct ggc atg cgg act gaa gat ctc cca aag gct gtg gtg ttc 99
Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe
15 20 25

ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg 147
Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
30 35 40 45

aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt 195
Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
50 55 60

cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac 243
His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
65 70 75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc 291
Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
80 85 90

tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg 339
Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
95 100 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac 387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His
110 115 120 125

ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat 435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr
130 135 140

tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc 483
Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe
145 150 155

tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg 531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg
160 165 170

ggg ctt ttt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc 579
Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr
175 180 185

atc act caa ggt ttg gca gtg tca acc atc tca tca ttc ttt cca cct 627
Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro
190 195 200 205

```
ggg tac caa gtc tct ttc tgc ttg gtg atg gta ctc ctt ttt gca gtg   675
Gly Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val
                210                 215                 220

gac aca gga cta tat ttc tct gtg aag aca aac att cga agc tca aca   723
Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr
            225                 230                 235

aga gac tgg aag gac cat aaa ttt aaa tgg aga aag gac cct caa gac   771
Arg Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp
        240                 245                 250

aaa tgaccccagg atcc                                              788
Lys
```

<210> 47
<211> 254
<212> PRT
<213> Homo sapiens

<400> 47

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
  1               5                  10                  15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
             20                  25                  30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
         35                  40                  45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
     50                  55                  60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65                  70                  75                  80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
                 85                  90                  95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
            100                 105                 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
        115                 120                 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
    130                 135                 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145                 150                 155                 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
                165                 170                 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
            180                 185                 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
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```
      195                 200                 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
    210                 215                 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225                 230                 235                 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
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<211> 788
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (13)..(774)

<400> 48

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gtt tca gct ggc atg cgg act gaa gat ctc cca aag gct gtg gtg ttc   99
Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe
     15                  20                  25

ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg   147
Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
 30                  35                  40                  45

aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt   195
Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
                 50                  55                  60

cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac   243
His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
             65                  70                  75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc   291
Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
         80                  85                  90

tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg   339
Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
     95                  100                 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac   387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His
110                 115                 120                 125

ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat   435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr
                130                 135                 140

tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc   483
Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe
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            145                 150                 155

tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg   531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg
        160                 165                 170

ggg ctt gtt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc   579
Gly Leu Val Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr
    175                 180                 185

atc act caa ggt ttg gca gtg tca acc atc tca tca ttc ttt cca cct   627
Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro
190                 195                 200                 205

ggg tac caa gtc tct ttc tgc ttg gtg atg gta ctc ctt ttt gca gtg   675
Gly Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val
                210                 215                 220

gac aca gga cta tat ttc tct gtg aag aca aac att cga agc tca aca   723
Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr
            225                 230                 235

aga gac tgg aag gac cat aaa ttt aaa tgg aga aag gac cct caa gac   771
Arg Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp
        240                 245                 250

aaa tgaccccagg atcc                                              788
Lys
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<210> 49
<211> 254
<212> PRT
<213> Homo sapiens

<400> 49

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
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Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
             20                  25                  30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
         35                  40                  45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
     50                  55                  60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65                  70                  75                  80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
                 85                  90                  95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
            100                 105                 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
        115                 120                 125
```

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His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
    130                 135                 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145                 150                 155                 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
                165                 170                 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
            180                 185                 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
        195                 200                 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
    210                 215                 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225                 230                 235                 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
                245                 250
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<210> 51
<211> 620
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (13)..(609)

<400> 51
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1 5 10

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gtt tca gct ggc atg cgg act gaa gat ctc cca aag gct gtg gtg ttc   99
Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe
     15                  20                  25

ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg   147
Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
 30                  35                  40                  45

aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt   195
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Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
                50                  55                  60

cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac   243
His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
            65                  70                  75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc   291
Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
        80                  85                  90

tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg   339
Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
    95                  100                 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac   387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His
110                 115                 120                 125

ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat   435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr
                130                 135                 140

tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc   483
Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe
            145                 150                 155

tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg   531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg
        160                 165                 170

ggg ctt ttt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc   579
Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr
    175                 180                 185

atc act caa ggt cat cat cat cat cat cat tgacaggatc c             620
Ile Thr Gln Gly His His His His His His
190                 195


<210> 52
<211> 199
<212> PRT
<213> Homo sapiens

<400> 52
Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
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Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
            20                  25                  30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
        35                  40                  45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
    50                  55                  60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65                  70                  75                  80
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Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
                 85                  90                  95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
            100                 105                 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
        115                 120                 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
    130                 135                 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145                 150                 155                 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
                165                 170                 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
            180                 185                 190

Gly His His His His His His
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<210> 53
<211> 620
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (13)..(609)

<400> 53

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                1                               5                  10

gtt tca gct ggc atg cgg act gaa gat ctc cca aag gct gtg gtg ttc   99
Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe
     15                  20                  25

ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg   147
Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
 30                  35                  40                  45

aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt   195
Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
                 50                  55                  60

cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac   243
His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
             65                  70                  75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc   291
Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
         80                  85                  90
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tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg   339
Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
 95                 100                 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac   387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His
110                 115                 120                 125

ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat   435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr
                130                 135                 140

tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc   483
Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe
            145                 150                 155

tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg   531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg
        160                 165                 170

ggg ctt gtt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc   579
Gly Leu Val Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr
    175                 180                 185

atc act caa ggt cat cat cat cat cat cat tgacaggatc c             620
Ile Thr Gln Gly His His His His His His
190                 195
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<210> 54
<211> 199
<212> PRT
<213> Homo sapiens

<400> 54

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
  1               5                  10                  15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
             20                  25                  30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
         35                  40                  45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
     50                  55                  60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65                  70                  75                  80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
                 85                  90                  95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
            100                 105                 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
        115                 120                 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
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130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

Gly His His His His His His
195

<210> 55
<211> 9196
<212> DNA
<213> Cricetulus griseus

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atttacatta taattgtaag taaaaatttt cagcctattt tgttatacat ttttgcgtaa 180

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cagcaaagtg ttattaattc atatgtccat atttcaattt tttatgaatt attaaattga 420

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gatgagtctt gtgaccttag tttctttaaa aacacaaaat tcttggaatg tgttttcatg 660

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caataatttt caaaagcagt tacccaactt tccaaataca atctgcagtt ttcttgatat 5700

gtgataaatt tagacaaaga aatagcacat tttaaaatag ctatttactc ttgatttttt 5760

tttcaaattt aggctagttc actagttgtg tgtaaggtta tggctgcaaa catctttgac 5820

tcttggttag ggaatccagg atgatttacg tgtttggcca aaatcttgtt ccattctggg 5880

tttcttctct atctaggtag ctagcacaag ttaaaggtgt ggtagtattg gaaggctctc 5940

aggtatatat ttctatattc tgtatttttt tcctctgtca tatatttgct ttctgtttta 6000

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tgttctaaga tttcttagca agttcatatc actgatttta acagttgctt cttttgtaat 6120

atagactgaa tgccccttat ttgaaatgct tgggatcaga aactcagatt tgaacttttc 6180

ttttttaata tttccatcaa gtttaccagc tgaatgtcct gatccaagaa tatgaaatct 6240

gaaatgcttt gaaatctgaa acttttagag tgataaagct tccctttaaa ttaatttgtg 6300

ttctatattt tttgacaatg tcaacctttc attgttatcc aatgagtgaa catattttca 6360

atttttttgt ttgatctgtt atattttgat ctgaccatat ttataaaatt ttatttaatt 6420

tgaatgttgt gctgttactt atctttatta ttatttttgc ttattttcta gccaaatgaa 6480

attatattct gtattatttt agtttgaatt ttactttgtg gcttagtaac tgccttttgt 6540

tggtgaatgc ttaagaaaaa cgtgtggtct actgatattg gttctaatct tatatagcat 6600

gttgtttgtt aggtagttga ttatgctggt cagattgtct tgagtttatg caaatgtaaa 6660

atatttagat gcttgttttg ttgtctaaga acaaagtatg cttgctgtct cctatcggtt 6720

ctggtttttc cattcatctc ttcaagctgt tttgtgtgtt gaatactaac tccgtactat 6780

cttgttttct gtgaattaac ccctttcaa aggtttcttt tctttttttt tttaagggac 6840

aacaagttta ttcagattac attttaagct gataatgtat gattgcaagg ttatcaacat 6900

ggcagaaatg tgaagaagct aggcacatta catccacatg gagtcaagag cagagagcag 6960

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atcaaccaag gcacatccac aggaaaaact gatttagaca acctctcatt gagactcttc 7140

ccagatgatt agactgtgtc aagttgacaa ttaaaactat cacacctgaa gccatcacta 7200

gtaaatataa tgaaaatgtt gattatcacc ataattcatc tgtatccctt tgttattgta 7260

gattttgtga agttcctatt caagtccctg ttccttcctt aaaaacctgt tttttagtta 7320

aataggtttt ttagtgttcc tgtctgtaaa tacttttta aagttagata ttattttcaa 7380

gtatgttctc ccagtctttg gcttgtattt tcatcccttc aatacatata tttttgtaat 7440

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tgtccggacc tccaaactga cttcctcctt cagggagtct ggaacagttc tatgctggtt 7800

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ccagagttca gctcagtgtt tagctgtggg tgtctgcatc tgcttccatc agctactgga 7980

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acagtgacag aattctcttt aaacctataa tggctccctc tgtggtggta tccctttttct 8160

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aatatgctta tatcaggttt attttggcta gtatttgtat gtgtttggtt agtgttttta 8400

accttaattg acatgtatcc ttatatttag acacagattt aaatatttga agtttttttt 8460

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caccagatct cattcaaggt ggttgtgagc caccatgtgg ttgctgggaa ttgaactcag 8580

gacctctgga agaacagtca gtgctcttaa ccgctgagcc atctctccag cccctgaagt 8640

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gtgttgacta catgtatgtc tgtgcaccat gtgctgacct ggtcttggcc agaagaaggt 8940

gtcatattct ctgaaactgg tattgtggat gttacgaact gccatagggt gctaggaatc 9000

aaaccccagc tcctctggaa aagcagccac tgctctgagc cactgagtcc tctcttcaag 9060

caggtgatgc caacttttaa tggttaccag tggataagag tgcttgtatc tctagcaccc 9120

atgaaaattt atgcattgct atatgggctt gtcacttcag cattgtgtga cagagacagg 9180

aggatcccaa gagctc 9196

<210> 56
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 56
gagacttcag cccacttcaa ttattggc 28

<210> 57
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 57
cttgtgtgac tcttaactct cagag 25

<210> 58
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 58
gaggccactt gtgtagcgcc aagtg 25

<210> 59
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 59
ccctcgagat aacttcgtat agc 23

<210> 60
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 60
ggtaggcctc actaactg 18

<210> 61
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 61
catagaaaca agtaacaaca gccag 25

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 62
gtgagtccat ggctgtcact g 21

<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 63
cctgacttgg ctattctcag 20

<210> 64
<211> 235
<212> PRT
<213> Homo sapiens

<400> 64
Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
20 25 30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
180 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225 230

<210> 65

<211> 92
<212> PRT
<213> Homo sapiens

<400> 65
Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His
1 5 10 15

Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys
20 25 30

Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser
35 40 45

Phe Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile
50 55 60

Tyr Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro
65 70 75 80

Asn Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val
85 90

<210> 66
<211> 5
<212> PRT
<213> Mus musculus

<400> 66
Ser Tyr Gly Met Ser
1 5

<210> 67
<211> 17
<212> PRT
<213> Mus musculus

<400> 67
Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 68
<211> 11
<212> PRT
<213> Mus musculus

<400> 68
Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr
1 5 10

<210> 69
<211> 10
<212> PRT
<213> Mus musculus

<400> 69
Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 70
<211> 7
<212> PRT
<213> Mus musculus

<400> 70
Asp Thr Ser Lys Leu Ala Ser
1 5

<210> 71
<211> 9
<212> PRT
<213> Mus musculus

<400> 71
Gln Gln Trp Ser Ser Asn Pro Pro Thr
1 5

<210> 72
<211> 120
<212> PRT
<213> Mus musculus

<400> 72
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 73
<211> 109
<212> PRT

<213> Mus musculus

<400> 73
Asp Ile Glu Leu Thr Gln Ser Pro Ser Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Arg Thr Lys Leu Glu Leu Lys Arg Ala Ala
100 105

<210> 74
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Amino Acid Sequence of Single Chain Antibody Fv

<400> 74
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser

130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr
165 170 175

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Trp Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala

<210> 75
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Amino Acid Sequence of Bispecific Single Chain Antibody

<400> 75
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser
130 135 140

```
Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala
145                 150                 155                 160

Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr
                165                 170                 175

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
            180                 185                 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
        195                 200                 205

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Trp Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu
225                 230                 235                 240

Lys Arg Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln
            260                 265                 270

Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
        275                 280                 285

Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His
    290                 295                 300

Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile Gly Tyr Phe
305                 310                 315                 320

Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe Lys Gly Lys
                325                 330                 335

Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Val Gln Leu
            340                 345                 350

Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr Arg Ser
        355                 360                 365

Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
385                 390                 395                 400

Ile Val Met Ser Gln Ser Pro Ser Ser Leu Pro Val Ser Val Gly Glu
                405                 410                 415

Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Gly
            420                 425                 430

Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
        435                 440                 445

Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val Pro
    450                 455                 460
```

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Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile
465                 470                 475                 480

Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln Tyr
                485                 490                 495

Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Val Leu Lys
            500                 505                 510

Arg Ala Ala
        515
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<210> 76
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Amino Acid Sequence of Bispecific Single Chain Antibody

<400> 76

```
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
  1               5                  10                  15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
             20                  25                  30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
         35                  40                  45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
     50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65                  70                  75                  80

Val Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                 85                  90                  95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
            100                 105                 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Pro Val Ser
    130                 135                 140

Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu
145                 150                 155                 160

Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser
            180                 185                 190

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205
```

```
Leu Ser Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
225                 230                 235                 240

Val Leu Lys Arg Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
            260                 265                 270

Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        275                 280                 285

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly
    290                 295                 300

Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val Ala
305                 310                 315                 320

Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
                325                 330                 335

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
            340                 345                 350

Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala
        355                 360                 365

Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro Gly
    370                 375                 380

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
385                 390                 395                 400

Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser Ile
                405                 410                 415

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
            420                 425                 430

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
        435                 440                 445

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
    450                 455                 460

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
465                 470                 475                 480

Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
                485                 490                 495

Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu Lys
            500                 505                 510

Arg Ala Ala
        515
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<210> 77
<211> 89
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 77
gaattcgacc cctcaccatg gaatggagct gggtctttct cttcttcctg tcagtaacta 60

ccggtgggga tccccactag tcctccgga 89

<210> 78
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 78
aattcgaccc ctcaccatgg aatggagctg ggtctttctc ttcttcctgt cagtaactac 60

cggtggggat ccccactagt cct 83

<210> 79
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 79
ccggaggact agtggggatc cccaccggta gttactgaca ggaagaagag aaagacccag 60

ctccattcca tggtgagggg tcg 83

<210> 80
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 80
gcgaccggtg tccactccca ggtccaactg caggagtcag gaggaggctt agtgcagcct 60

ggagggtccc tgaaactctc ctgtgcagcc tctggattca ctttcagtag ctatggcatg 120

tcttgggttc gccagactcc agacaagagg ctggagttgg tcgcaaccat taatagtaat 180

ggtggtagca cctattatcc agacagtgtg aagggccgat tcaccatctc cagagacaat 240

gccaagaaca ccctgtacct gcaaatgagc agtctgaagt ctgaggacac agccatgtat 300

tactgtgcaa gagatcggga tggttacgac gagggatttg actactgggg cccagggacc 360

acggtcaccg tctcctcagg tggcggaggc agcggaggcg gtggatcccg c 411

<210> 81
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 81
gcgaccggtg tccactccca ggtccaactg caggagtcag gaggaggctt agtgcagcct 60

ggagggtccc tgaaactctc ctgtgcagcc tctggattca ctttcagtag ctatggcatg 120

<210> 82
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 82
cggcccttca cactgtctgg ataataggtg ctaccaccat tactattaat ggttgcgacc 60

aactccagcc tcttgtctgg agtctggcga acccaagaca tgccatagct actgaaagtg 120

<210> 83
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 83
ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 60

ctgcaaatga gcagtctgaa gtctgaggac acagccatgt attactgtgc aagagatc 118

<210> 84
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 84
cgcggatcca ccgcctccgc tgcctccgcc acctgaggag acggtgaccg tggtccctgg 60

gccccagtag tcaaatccct cgtcgtaacc atcccgatct cttgcacagt aatacatg 118

<210> 85
<211> 386
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 85
gcgggatccg gtggcggagg ctcggacatt gagctgaccc aatctccatc aatcatgtct 60

gcatctccag gggagaaggt caccatgacc tgcagtgcca gctcaagtgt aagttacatg 120

cactggtacc agcagaagtc aggcacctcc cccaaaagat ggatttatga cacatccaaa 180

ctggcttctg gagtccctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 240

acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtggagtagt 300

aacccaccca cgttcggagg gcggaccaag ctggaactga aacgggccgc cgagcccaaa 360

tctcctgaca aaactcacac gtggcg 386

<210> 86
<211> 109
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 86
gcgggatccg gtggcggagg ctcggacatt gagctgaccc aatctccatc aatcatgtct 60

gcatctccag gggagaaggt caccatgacc tgcagtgcca gctcaagtg 109

<210> 87
<211> 111
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 87
gcagggactc cagaagccag tttggatgtg tcataaatcc atcttttggg ggaggtgcct 60

gacttctgct ggtaccagtg catgtaactt acacttgagc tggcactgca g 111

<210> 88
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 88
ctggcttctg gagtccctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 60

acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtgg 114

<210> 89
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 89
cgccacgtgt gagttttgtc aggagatttg ggctcggcgg cccgtttcag ttccagcttg 60

gtccgccctc cgaacgtggg tgggttacta ctccactgct ggcagtaata agtg 114

<210> 90
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 90
gcgggatccg gtggcggagg ctcggacatt gagctgaccc aatctccatc aatcatgtct 60

gcatctccag gggagaaggt caccatgacc tgcagtgcca gctcaagtgt aagttacatg 120

cactggtacc agcagaagtc aggcacctcc cccaaaagat ggatttatga cacatccaaa 180

ctggcttctg gagtccctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 240

acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtggagtagt 300

aacccaccca cgttcggagg gcggaccaag ctggaactga aacgggccgc cggtggcgga 360

ggcagcggag gcggtggtag cggtggcgga actagtgcg 399

<210> 91
<211> 127
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 91
cgcactagtt ccgccaccgc taccaccgcc tccgctgcct ccgccaccgg cggcccgttt 60

cagttccagc ttggtccgcc ctccgaacgt gggtgggtta ctactccact gctggcagta 120

ataagtg 127

<210> 92
<211> 812
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 92
tttactagtg gtggcggagg cagcggaggc ggtggtagcc aggttcagtt gcagcagtct 60

gacgctgagt tggtgaaacc tggggcttca gtgaagattt cctgcaaggc ttctggctac 120

accttcactg accatgcaat tcactgggtg aaacagaacc ctgaacaggg cctggaatgg 180

attggatatt tttctcccgg aaatgatgat tttaaataca atgagaggtt caagggcaag 240

gccacactga ctgcagacaa atcctccagc actgcctacg tgcagctcaa cagcctgaca 300

tctgaggatt ctgcagtgta tttctgtacc agatccctga atatggccta ctggggtcaa 360

ggaacctcag tcaccgtctc ctcaggtggc ggaggcagcg gaggcggtgg ctccggaggc 420

ggaggctcgg acattgtgat gtcacagtct ccatcctccc tacctgtgtc agttggcgag 480

aaggttactt tgagctgcaa gtccagtcag agccttttat atagtggtaa tcaaaagaac 540

tacttggcct ggtaccagca gaaaccaggg cagtctccta aactgctgat ttactgggca 600

tccgctaggg aatctggggt ccctgatcgc ttcacaggca gtggatctgg gacagatttc 660

actctctcca tcagcagtgt gaagactgaa gacctggcag tttattactg tcagcagtat 720

tatagctatc ccctcacgtt cggtgctggg accaagctgg tgctgaaacg ggccgccgag 780

cccaaatctc ctgacaaaac tcacacgtgc cc 812

<210> 93
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 93
tttactagtg gtggcggagg cagcggaggc ggtggtagcc aggttcagtt gcagcagtct 60

gacg 64

<210> 94
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 94
gggcacgtgt gagttttgtc agg 23

<210> 95
<211> 817
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 95
cttcctgtca gtaactaccg gtgtccactc ccaggttcag ttgcagcagt ctgacgctga 60

gttggtgaaa cctggggctt cagtgaagat ttcctgcaag gcttctggct acaccttcac 120

tgaccatgca attcactggg tgaaacagaa ccctgaacag ggcctggaat ggattggata 180

tttttctccc ggaaatgatg attttaaata caatgagagg ttcaagggca aggccacact 240

gactgcagac aaatcctcca gcactgccta cgtgcagctc aacagcctga catctgagga 300

ttctgcagtg tatttctgta ccagatccct gaatatggcc tactggggtc aaggaacctc 360

agtcaccgtc tcctcaggtg gcggaggcag cggaggcggt ggctccggag gcggaggctc 420

ggacattgtg atgtcacagt ctccatcctc cctacctgtg tcagttggcg agaaggttac 480

tttgagctgc aagtccagtc agagcctttt atatagtggt aatcaaaaga actacttggc 540

ctggtaccag cagaaaccag ggcagtctcc taaactgctg atttactggg catccgctag 600

ggaatctggg gtccctgatc gcttcacagg cagtggatct gggacagatt tcactctctc 660

catcagcagt gtgaagactg aagacctggc agtttattac tgtcagcagt attatagcta 720

tcccctcacg ttcggtgctg ggaccaagct ggtgctgaaa cgggccgccg gtggcggagg 780

cagcggaggc ggtggtagcg gtggcggaac tagtaaa 817

<210> 96
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 96
cttcctgtca gtaactaccg gtgtccactc ccaggttcag 40

<210> 97
<211> 85

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 97
tttactagtt ccgccaccgc taccaccgcc tccgctgcct ccgccaccgg cggcccgttt 60

cagcaccagc ttggtcccag caccg 85

<210> 98
<211> 806
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 98
tttactagtg gtggcggagg cagcggaggc ggtggtagcc aggtccaact gcaggagtca 60

ggaggaggct tagtgcagcc tggagggtcc ctgaaactct cctgtgcagc ctctggattc 120

actttcagta gctatggcat gtcttgggtt cgccagactc cagacaagag gctggagttg 180

gtcgcaacca ttaatagtaa tggtggtagc acctattatc cagacagtgt gaagggccga 240

ttcaccatct ccagagacaa tgccaagaac accctgtacc tgcaaatgag cagtctgaag 300

tctgaggaca cagccatgta ttactgtgca agagatcggg atggttacga cgagggattt 360

gactactggg gcccagggac cacggtcacc gtctcctcag gtggcggagg cagcggaggc 420

ggtggatccg gtggcggagg ctcggacatt gagctgaccc aatctccatc aatcatgtct 480

gcatctccag gggagaaggt caccatgacc tgcagtgcca gctcaagtgt aagttacatg 540

cactggtacc agcagaagtc aggcacctcc cccaaaagat ggatttatga cacatccaaa 600

ctggcttctg gagtccctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 660

acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtggagtagt 720

aacccaccca cgttcggagg gcggaccaag ctggaactga aacgggccgc cgagcccaaa 780

tctcctgaca aaactcacac gtgccc 806

<210> 99
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequense: Synthetic DNA

<400> 99
tttactagtg gtggcggagg cagcggaggc ggtggtagcc aggtccaact gcaggagtca 60

ggagg 65

<210> 100
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 100
acaacggaat tcaagcctgt agcacatgtt gtagc 35

<210> 101
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 101
ggcgggatcc tcacagggca atgatcccaa agtagacct 39

<210> 102
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 102
aacaacggaa ttcgacccac ggctccaccc tctctcccct ggaaaggaca ccatgagcac 60

tgaaagcatg atccgggacg tggagctggc cgaggaggc 99

<210> 103
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 103
tgccacgatc aggaaggaga agaggctgag gaacaagcac cgcctggagc cctggggccc 60

ccctgtcttc ttggggagcg cctcctcggc cagctccac 99

<210> 104
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 104
tctccttcct gatcgtggca ggcgccacca cgctcttctg cctgctgcac tttggagtga 60

tcggccccca gagggaagag ttccccaggg acctctctc 99

<210> 105
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 105
ttggctacaa catgtgctac tgcctgggcc agagggctga ttagagagag gtccctgggg 60

aac 63

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 106
aacaacggaa ttcgacccac 20

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Synthetic DNA

<400> 107
ttggctacaa catgtgctac 20

<210> 108
<211> 717
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (46)..(708)

<400> 108
gaattcgacc cacggctcca ccctctctcc cctggaaagg acacc atg agc act gaa 57
Met Ser Thr Glu

```
agc atg atc cgg gac gtg gag ctg gcc gag gag gcg ctc ccc aag aag   105
Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala Leu Pro Lys Lys
  5                  10                  15                  20

aca ggg ggg ccc cag ggc tcc agg cgg tgc ttg ttc ctc agc ctc ttc   153
Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe Leu Ser Leu Phe
                25                  30                  35

tcc ttc ctg atc gtg gca ggc gcc acc acg ctc ttc tgc ctg ctg cac   201
Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe Cys Leu Leu His
            40                  45                  50

ttt gga gtg atc ggc ccc cag agg gaa gag ttc ccc agg gac ctc tct   249
Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro Arg Asp Leu Ser
        55                  60                  65

cta atc agc cct ctg gcc cag gca gta gca cat gtt gta gca aac cct   297
Leu Ile Ser Pro Leu Ala Gln Ala Val Ala His Val Val Ala Asn Pro
    70                  75                  80

caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc   345
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
85                  90                  95                  100

ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca   393
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
                105                 110                 115

gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc   441
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
            120                 125                 130

tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc   489
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
        135                 140                 145

gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc   537
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
    150                 155                 160

tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag   585
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
165                 170                 175                 180

ccc atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc   633
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
                185                 190                 195

agc gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg   681
Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
            200                 205                 210

cag gtc tac ttt ggg atc att gcc ctg tgaggatcc                    717
Gln Val Tyr Phe Gly Ile Ile Ala Leu
        215                 220
```

<210> 109

<211> 221
<212> PRT
<213> Homo sapiens

<400> 109
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Ala His Val
65 70 75 80

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
85 90 95

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
100 105 110

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
115 120 125

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
130 135 140

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
145 150 155 160

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
165 170 175

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
180 185 190

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
195 200 205

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215 220

<210> 110
<211> 383
<212> DNA
<213> Cricetulus griseus

<400> 110
gttaactggg gctcttttaa accctgaatt tttctaaatc cccacctcca agagtttggt 60

ttaaactgat ttttttaatg aataccttt gaagaataga gcattgtctc atcatgcaaa 120

gcttctcagg gattcagcta gcatgttgaa gaaacataag ggtgttaaat tgtttgtcac 180

aagtgctgaa taaatattga cgtagtcttc agctattcta tactggaagt agatgatatt 240

ctcattggaa attctgttag gaagtaaccc ttcttgtctt cttacctgca tagaatccca 300

ggatataaaa cttgtgcttg tcgcccttgc cattgtctct cactggtggc ctttattgca 360

tctcatatct gccttctctt tcc 383

<210> 111
<211> 564
<212> DNA
<213> Cricetulus griseus

<400> 111
taagaattcc tgtgcccagc tgtatgtgag gctctctgca ggtgtaggga tgtttctgct 60

ttctttctgc acatgcttca cagctgaagt cctttgggtg tgagattgac attcagatag 120

actaaagtga ctggacttgt tgggaaacat actgtatgca ttattgccgt tgcctccagg 180

tgaaattaac acctcattca ccaatccctg ttcatccaaa ctttctaccc acatcacttt 240

aaatagaaat tagacccaat atgactcctt ttttcctaag ctgtttatag agattgtgct 300

ggagcagtga gcttttgtgt ttgtttgttt gttttgtaat tttccccatg aaaatttctc 360

taaactcaaa cctaagaggg aaaaaaaaaa aacagactta tatgtgccac acttgtaaaa 420

aaaaatcatg aaagatgtat atgatatttt taaacagttt gaatattaag atcacaattt 480

ctattttaaa aacaatcttg ttttacatat caatcaccca attcccttgc cttcccatcc 540

tcccattccc cccactgatc cccc 564

<210> 112
<211> 120
<212> DNA
<213> Cricetulus griseus

<400> 112
atgaatgttc attctttggg tatatgccca agagtagaat tgctaaatat tgaggtagac 60

tgattcccat tttcttgagg agtcgccata ttgatttcca aagtgactgt acaagttaac 120

<210> 113
<211> 274
<212> DNA
<213> Cricetulus griseus

<400> 113
aggcactagg taaatatttt tgaagaaaga atgagtatct cctatttcag aaaaactttt 60

attgacttaa atttaggata tcagaattag aaaacagtaa aaatttatag gagagttttt 120

aatgaatgtt attttaaggt tccatacaaa tagtaattaa aacttacaca aactatttgt 180

agtaatgatt cagtctggta taccctgatg agcattatac acttttaaat tctttttgta 240

aatttttta ttagttcaaa ttaggaacaa gctt 274